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OIPE

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JAN 18 2002

TECH CENTER 1600/2900

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/944,896

DATE: 01/07/2002

TIME: 16:28:51

Input Set : N:\Crf3\RULE60\09944896.raw

Output Set: N:\CRF3\01072002\I944896.raw

1 &lt;110&gt; APPLICANT: Baker, Kevin

2 Botstein, David

3 Eaton, Dan

4 Ferrara, Napoleone

5 Filvaroff, Ellen

6 Gerritsen, Mary

7 Goddard, Audrey

8 Godowski, Paul

9 Grimaldi, Christopher

10 Gurney, Austin

11 Hillan, Kenneth

12 Kljavin, Ivar

13 Napier, Mary

14 Roy, Margaret

15 Tumas, Daniel

16 Wood, William

17 <120> TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
18 ACIDS ENCODING THE SAME

19 &lt;130&gt; FILE REFERENCE: P2548P1C1

20 &lt;140&gt; CURRENT APPLICATION NUMBER: 09/944,896

21 &lt;141&gt; CURRENT FILING DATE: 2001-08-31

22 &lt;150&gt; PRIOR APPLICATION NUMBER: 09/866,028

23 &lt;151&gt; PRIOR FILING DATE: 2001-05-25

27 &lt;160&gt; NUMBER OF SEQ ID NOS: 120

29 &lt;210&gt; SEQ ID NO: 1

30 &lt;211&gt; LENGTH: 2454

31 &lt;212&gt; TYPE: DNA

32 &lt;213&gt; ORGANISM: Homo Sapien

33 &lt;400&gt; SEQUENCE: 1

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34 ggactaatct gtgggagcag tttattccag tatcaccag ggtgcagcca 50
35 caccaggact gtgttgaagg gtgttttttt tcttttaaata gtaatacctc 100
36 ctcatctttt cttottacac agtgtctgag aacatttaca ttatagataa 150
37 gtagtacatg gtggataact tctactttta ggaggactac tctcttctga 200
38 cagtccatga ctggtcttct acactaagac accatgaagg agtatgtgct 250
39 cctattattc ctggctttgt gctctgccaa acccttcttt agcccttcac 300
40 acatcgact gaagaatatg atgctgaagg atatggaaga cacagatgat 350
41 gatgatgatg atgatgatga tgatgatgat gatgaggaca actctctttt 400
42 tccaacaaga gagccaagaa gccatttttt tccatttgat ctgtttccaa 450
43 tgtgtccatt tggatgtcag tgctattcac gagttgtaca ttgctcagat 500
44 ttaggtttga cctcagtcac aaccaacatt ccatttgata ctggaatgct 550
45 tgatcttcaa aacaataaaa ttaaggaaat caaagaaaat gattttaaag 600
46 gactcacttc actttatggt ctgatcctga acaacaacaa gctaacgaag 650
47 attcacccaa aagcctttct aaccacaaag aagttgcgaa ggctgtatct 700
48 gtcccacaat caactaagt aaataccact taatcttccc aaatcattag 750
49 cagaactcag aattcatgaa aataaagta agaaaataca aaaggacaca 800
50 ttcaaaggaa tgaatgcttt acacgttttg gaaatgagtg caaacctct 850
51 tgataataat gggatagagc caggggcatt tgaaggggtg acggtgttcc 900

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52  atatcagaat tgcagaagca aaactgacct cagttcctaa aggcctacca 950
53  ccaactttat tggagcttca cttagattat aataaaatTTT caacagtggg 1000
54  acttgaggat tttaaacgat acaaagaact acaaaggctg ggcctaggaa 1050
55  acaacaaaat cacagatata gaaaatggga gtcttgctaa cataccacgt 1100
56  gtgagagaaa tacatttgga aaacaataaa ctaaaaaaa tcccttcagg 1150
57  attaccagag ttgaaatacc tccagataat ctcccttcac tctaattcaa 1200
58  ttgcaagagt gggagtaaat gacttctgtc caacagtgcc aaagatgaag 1250
59  aaatctttat acagtgcatt aagtttattc aacaacccgg tgaaatactg 1300
60  ggaaatgcaa cctgcaacat ttcgttgtgt tttgagcaga atgagtgttc 1350
61  agcttgggaa ctttggaatg taataattag taattggtaa tgtccattta 1400
62  atataagatt caaaaatccc tacatttgga atacttgaa tctattaata 1450
63  atggtagtat tatatatata agcaaatatc tattctcaag tggtaaagtcc 1500
64  actgacttat tttatgacaa gaaatttcaa cggaattttg ccaaactatt 1550
65  gatacataag gggttgagag aaacaagcat ctattgcagt ttcctttttg 1600
66  cgtacaaatg atcttacata aatctcatgc ttgaccattc ctttcttcac 1650
67  aacaaaaaag taagatatcc ggtatttaac actttgttat caagcacatt 1700
68  ttaaaaagaa ctgtactgta aatggaatgc ttgacttagc aaaatttgtg 1750
69  ctctttcatt tgctgttaga aaaacagaat taacaaagac agtaatgtga 1800
70  agagtgcatt acactattct tattctttag taacttgggt agtactgtaa 1850
71  tatttttaat catcttaaag tatgatttga tataatctta ttgaaattac 1900
72  cttatcatgt cttagagccc gtctttatgt ttaaaactaa tttcttaaaa 1950
73  taaagccttc agtaaatgtt cattaccaac ttgataaatg ctactcataa 2000
74  gagctggttt ggggctatag catatgcttt ttttttttta attattacct 2050
75  gatttaaaaa tctctgtaaa aacgtgtagt gtttcataaa atctgtaact 2100
76  cgcattttta tgatccgcta ttataagctt ttaatagcat gaaaattgtt 2150
77  aggcctatata acattgccac ttcaactcta aggaatattt ttgagataac 2200
78  cctttggaag accttgcttg gaagagcctg gacactaaca attctacacc 2250
79  aaattgtctc ttcaaatacg tatggactgg ataactctga gaaacacatc 2300
80  tagtataact gaataagcag agcatcaaat taaacagaca gaaaccgaaa 2350
81  gctctatata aatgctcaga gttctttatg tatttcttat tggcattcaa 2400
82  catatgtaaa atcagaaaac agggaaattt tcattaaaaa tattgggttg 2450
83  aaat 2454

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85 &lt;210&gt; SEQ ID NO: 2

86 &lt;211&gt; LENGTH: 379

87 &lt;212&gt; TYPE: PRT

88 &lt;213&gt; ORGANISM: Homo Sapien

89 &lt;400&gt; SEQUENCE: 2

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90  Met Lys Glu Tyr Val Leu Leu Leu Phe Leu Ala Leu Cys Ser Ala
91      1              5              10              15
92  Lys Pro Phe Phe Ser Pro Ser His Ile Ala Leu Lys Asn Met Met
93              20              25              30
94  Leu Lys Asp Met Glu Asp Thr Asp Asp Asp Asp Asp Asp Asp
95              35              40              45
96  Asp Asp Asp Asp Asp Glu Asp Asn Ser Leu Phe Pro Thr Arg Glu
97              50              55              60
98  Pro Arg Ser His Phe Phe Pro Phe Asp Leu Phe Pro Met Cys Pro
99              65              70              75
100  Phe Gly Cys Gln Cys Tyr Ser Arg Val Val His Cys Ser Asp Leu
101              80              85              90

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102      Gly Leu Thr Ser Val Pro Thr Asn Ile Pro Phe Asp Thr Arg Met
103                      95                      100                      105
104      Leu Asp Leu Gln Asn Asn Lys Ile Lys Glu Ile Lys Glu Asn Asp
105                      110                      115                      120
106      Phe Lys Gly Leu Thr Ser Leu Tyr Gly Leu Ile Leu Asn Asn Asn
107                      125                      130                      135
108      Lys Leu Thr Lys Ile His Pro Lys Ala Phe Leu Thr Thr Lys Lys
109                      140                      145                      150
110      Leu Arg Arg Leu Tyr Leu Ser His Asn Gln Leu Ser Glu Ile Pro
111                      155                      160                      165
112      Leu Asn Leu Pro Lys Ser Leu Ala Glu Leu Arg Ile His Glu Asn
113                      170                      175                      180
114      Lys Val Lys Lys Ile Gln Lys Asp Thr Phe Lys Gly Met Asn Ala
115                      185                      190                      195
116      Leu His Val Leu Glu Met Ser Ala Asn Pro Leu Asp Asn Asn Gly
117                      200                      205                      210
118      Ile Glu Pro Gly Ala Phe Glu Gly Val Thr Val Phe His Ile Arg
119                      215                      220                      225
120      Ile Ala Glu Ala Lys Leu Thr Ser Val Pro Lys Gly Leu Pro Pro
121                      230                      235                      240
122      Thr Leu Leu Glu Leu His Leu Asp Tyr Asn Lys Ile Ser Thr Val
123                      245                      250                      255
124      Glu Leu Glu Asp Phe Lys Arg Tyr Lys Glu Leu Gln Arg Leu Gly
125                      260                      265                      270
126      Leu Gly Asn Asn Lys Ile Thr Asp Ile Glu Asn Gly Ser Leu Ala
127                      275                      280                      285
128      Asn Ile Pro Arg Val Arg Glu Ile His Leu Glu Asn Asn Lys Leu
129                      290                      295                      300
130      Lys Lys Ile Pro Ser Gly Leu Pro Glu Leu Lys Tyr Leu Gln Ile
131                      305                      310                      315
132      Ile Phe Leu His Ser Asn Ser Ile Ala Arg Val Gly Val Asn Asp
133                      320                      325                      330
134      Phe Cys Pro Thr Val Pro Lys Met Lys Lys Ser Leu Tyr Ser Ala
135                      335                      340                      345
136      Ile Ser Leu Phe Asn Asn Pro Val Lys Tyr Trp Glu Met Gln Pro
137                      350                      355                      360
138      Ala Thr Phe Arg Cys Val Leu Ser Arg Met Ser Val Gln Leu Gly
139                      365                      370                      375
140      Asn Phe Gly Met
142 <210> SEQ ID NO: 3
143 <211> LENGTH: 20
144 <212> TYPE: DNA
145 <213> ORGANISM: Artificial Sequence
146 <220> FEATURE:
147 <223> OTHER INFORMATION: Synthetic Oligonucleotide Probe
148 <400> SEQUENCE: 3
149      ggaaatgagt gcaaaccctc 20
151 <210> SEQ ID NO: 4
152 <211> LENGTH: 24

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153 <212> TYPE: DNA
154 <213> ORGANISM: Artificial Sequence
155 <220> FEATURE:
156 <223> OTHER INFORMATION: Synthetic Oligonucleotide Probe
157 <400> SEQUENCE: 4
158      tcccaagctg aacactcatt ctgc 24
160 <210> SEQ ID NO: 5
161 <211> LENGTH: 50
162 <212> TYPE: DNA
163 <213> ORGANISM: Artificial Sequence
164 <220> FEATURE:
165 <223> OTHER INFORMATION: Synthetic Oligonucleotide Probe
166 <400> SEQUENCE: 5
167      ggggtgacggt gttccatatc agaattgcag aagcaaaact gacctcagtt 50
169 <210> SEQ ID NO: 6
170 <211> LENGTH: 3441
171 <212> TYPE: DNA
172 <213> ORGANISM: Homo Sapien
173 <400> SEQUENCE: 6
174      cggacgcgtg ggcggacgcg tgggcccgcg gcaccgcccc cggcccggcc 50
175      ctccgccttc cgcactcgcg cctccctccc tccgcccgtt cccgcgccct 100
176      cctccctccc tctcccccag ctgtcccgtt cgcgtcatgc cgagcctccc 150
177      ggccccgcgc gccccgctgc tgctcctcgg gctgctgctg ctcggtctcc 200
178      ggccggcccg cggcgccggc ccagagcccc ccgtgctgcc catccgttct 250
179      gagaaggagc cgctgcccgt tcggggagcg gcaggctgca ccttcggcgg 300
180      gaaggtctat gccttgagcg agacgtggca cccggacctt gggcagccat 350
181      tcgggggatg gcgctgcgtg ctgtgcgcct gcgaggcgcc tcagtggggt 400
182      cgccgtacca ggggcccttg cagggtcagc tgcaagaaca tcaaaccaga 450
183      gtgcccacc ccggcctgtg ggcagccgcg ccagctgccg ggacactgct 500
184      gccagacctg cccccaggag cgcagcagtt cggagcggca gccgagcgcc 550
185      ctgtccttcg agtatccgcg ggaccggag catcgcagtt atagcgaccg 600
186      cggggagcca ggcgctgagg agcgggcccg tggtgacggc cacacggact 650
187      tcgtggcgct gctgacaggg ccgaggtcgc aggcggtggc acgagcccga 700
188      gtctcgctgc tgcgctctag cctccgcttc tctatctcct acaggcggct 750
189      ggaccgccct accaggatcc gcttctcaga ctccaatggc agtgtcctgt 800
190      ttgagcacc tgcagcccc acccaagatg gcctggtctg tgggggtgtg 850
191      cgggcagtg ctcggttgtc tctgcggctc cttagggcag aacagctgca 900
192      tgtggcaact gtgacactca ctcacccttc aggggaggtc tgggggcctc 950
193      tcatccggca ccgggccctg gctgcagaga ccttcagtgc catcctgact 1000
194      ctagaaggcc cccacagca gggcgtaggg ggcacacccc tgcctactct 1050
195      cagtgcacac gaggactcct tgcatttttt gctgctcttc cgagggctgc 1100
196      tggaaaccag gagtggggga ctaaccaggg ttcccttgag gctccagatt 1150
197      ctacaccagg ggcagctact gcgagaactt caggccaatg tctcagccca 1200
198      ggaaccaggc tttgctgagg tgcgcccaca cctgacagtc caggagatgg 1250
199      actggctggg gctgggggag ctgcagatgg ccctggagtg ggcaggcagg 1300
200      ccagggctgc gcatcagtgg acacattgct gccaggaaga gctgcgacgt 1350
201      cctgcaaaagt gtcctttgtg gggctgatgc cctgatccca gtccagacgg 1400
202      gtgctgccgg ctcagccagc ctcacgctgc taggaaatgg ctccctgatc 1450
203      tatcaggtgc aagtggtagg gacaagcagt gaggtggtgg ccatgacact 1500

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204 ggagaccaag cctcagcgga gggatcagcg cactgtcctg tgccacatgg 1550
205 ctggactcca gccaggagga cacacggccg tgggtatctg ccctgggctg 1600
206 ggtgcccag gggctcatat gctgctgcag aatgagctct tcctgaacgt 1650
207 gggcaccaag gacttcccag acggagagct tcgggggcac gtggctgccc 1700
208 tgccctactg tgggcatagc gcccgccatg acacgctgcc cgtgccccta 1750
209 gcaggagccc tgggtgtacc ccctgtgaag agccaagcag caggggcacgc 1800
210 ctggctttcc ttggataccc actgtcacct gcactatgaa gtgctgtctgg 1850
211 ctgggcttgg tggctcagaa caaggcactg tcactgccc a cctccttggg 1900
212 cctcctggaa cgccagggcc tcggcggtg ctgaagggat tctatggctc 1950
213 agaggcccag ggtgtggtga aggacctgga gccggaaactg ctgcggcacc 2000
214 tggcaaaaag catggcctcc ctgatgatca ccaccaaggg tagccccaga 2050
215 ggggagctcc gagggcaggt gcacatagcc aaccaatgtg aggttggcgg 2100
216 actgcgcctg gaggcggccg gggccgaggg ggtgcgggcg ctgggggctc 2150
217 cggatacagc ctctgtctgc ccgctgtgg tgctgtgtct cccggcccta 2200
218 gcgcccacca aacctggtgg tcctgggcgg ccccgagacc ccaacacatg 2250
219 cttcttcgag gggcagcagc gccccacgg ggctcgtggt gcgcccact 2300
220 acgaccgcgt ctgtcactc tgcacctgcc agagacgaac ggtgatctgt 2350
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224 gaccggagct ggcgggcagc ggttacgcgg tggcaccgcc ttgtgcccc 2550
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231 ggtgcctcac tgtgagcggg atgactgttc actgccactg tcctgtggct 2900
232 cggggaagga gagtcatgc tgttcccgt gcacggccca ccggcgcccc 2950
233 ccagagacca gaactgatcc agagctggag aaagaagccg aaggctctta 3000
234 gggagcagcc agagggccaa gtgaccaaga ggatggggcc tgagctgggg 3050
235 aaggggtggc atcgaggacc ttcttgcatl ctctgtggg aagccagtg 3100
236 cctttgtccc tctgtcctgc ctctactccc acccccacta cctctgggaa 3150
237 ccacagctcc acaaggggga gaggcagctg ggccagaccg aggtcacagc 3200
238 cactccaagt cctgccctgc caccctcggc ctctgtcctg gaagccccac 3250
239 ccctttcttc ctgtacataa tgtactggc ttgttgggat ttttaattta 3300
240 tcttactca gcaccaagg ccccgacac tccactcctg ctgcccctga 3350
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242 tttcagtcaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 3441

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244 &lt;210&gt; SEQ ID NO: 7

245 &lt;211&gt; LENGTH: 954

246 &lt;212&gt; TYPE: PRT

247 &lt;213&gt; ORGANISM: Homo Sapien

248 &lt;400&gt; SEQUENCE: 7

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249 Met Pro Ser Leu Pro Ala Pro Pro Ala Pro Leu Leu Leu Gly
250 1 5 10 15
251 Leu Leu Leu Leu Gly Ser Arg Pro Ala Arg Gly Ala Gly Pro Glu
252 20 25 30
253 Pro Pro Val Leu Pro Ile Arg Ser Glu Lys Glu Pro Leu Pro Val

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## VERIFICATION SUMMARY

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